

Amendments to the Specification:

Please replace paragraph [0032] beginning at page 6, line 26, with the following:

--[0032] The term "EPHA2", "BAG4", or "ARF1" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of at least about 20, 50, 100, 200, 500, 1000, or more amino acids, to a EPHA2, BAG4, or ARF1 sequence of SEQ ID NO:2; 4, or 6; (2) bind to antibodies, *e.g.*, polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of ~~SEQ ID NO:2, 4, or 6, or 8,~~ SEQ ID NO:2, 4, or 6, or conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a EPHA2, BAG4, or ARF1 nucleic acid sequence of SEQ ID NO:1, 3, or 5, or conservatively modified variants thereof; or (4) or have a nucleic acid sequence that has greater than about 90%, preferably greater than about 96%, 97%, 98%, 99%, or higher nucleotide sequence identity, preferably over a region of over a region of at least about 30, 50, 100, 200, 500, 1000, or more nucleotides, to SEQ ID NO:1, 3, or 5; or (5) have at least 25, often 50, 75, 100, 150, 200, 250, 300, 350, 400 or more contiguous amino acid of SEQ ID NO:2, 4, or 6; or at least 25, often 50, 75, 100, 150, 200, 250, 300, 350, 400, 500, or more contiguous nucleotides of SEQ ID NO:1, 3, or 5. A EPHA2, BAG4, or ARF1 polynucleotide or polypeptide sequence is typically from a human, but may be from other mammals, but not limited to, a non-human primate, a rodent, *e.g.*, a rat, mouse, or hamster; a cow, a pig, a horse, a sheep, or other mammal. A "EPHA2", "BAG4", or "ARF1" polypeptide and a "EPHA2", "BAG4", or "ARF1" polynucleotide include both naturally occurring or recombinant forms.--

Please replace paragraph [0098] beginning at page 6, line 26, with the following:

--[0098] In another embodiment, amplification-based assays are used to measure the copy number of EPHA2, BAG4, or ARF1. In such an assay, the EPHA2, BAG4, or ARF1 nucleic acid sequences act as a template in an amplification reaction (*e.g.*, Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the copy number of the cancer-associated gene. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, *e.g.*, in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.). The known nucleic acid sequences for EPHA2, BAG4, or ARF1 (*see, e.g., SEQ ID NO:1, 3, or 7*) (*see, e.g., SEQ ID NO:1, 3, or 5*) is sufficient to enable one of skill to routinely select primers to amplify any portion of the gene.--

Please replace paragraph [0157] beginning at page 43, line 26, with the following:

--[0157] Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly-gly poly-Gly sequences of between about 5 and 200 amino acids (SEQ ID NO:7). Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.--

Please replace paragraph [0160] beginning at page 44, line 26, with the following:

--[0160] [0161] The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a EPHA2, BAG4, or ARF1 polypeptide into the computer

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system. The amino acid sequence may comprise ~~SEQ ID NO: 2, 4, or 8~~ SEQ ID NO.2, 4, or 6. The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*, magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.